IDH2 mutations are frequent in angioimmunoblastic T-cell lymphoma

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Abstract

Mutations in isocitrate dehydrogenase 1 (IDH1) and isocitrate dehydrogenase 2 (IDH2) occur in most grade 2 and 3 gliomas, secondary glioblastomas, and a subset of acute myelogenous leukemias, but have not been detected in other tumor types. The mutations occur at specific arginine residues, and result in the acquisition of a novel enzymatic activity that converts 2-oxoglutarate to D-2-hydroxyglutarate. This study reports IDH1 and IDH2 genotyping results from a set of lymphomas which included a large set of peripheral T-cell lymphomas (PTCL). IDH2 mutations were identified in approximately 20% of angioimmunoblastic T-cell lymphomas (AITL), but not in other PTCL entities. These results were confirmed in an independent set of AITL patients, where the IDH2 mutation rate was approximately 45%. This is the second common genetic lesion identified in AITL after TET2, and extends the number of neoplastic diseases where IDH1 and IDH2 mutations may play a role.

Introduction

Heterozygous isocitrate dehydrogenase 1 and 2 (IDH1 and IDH2) mutations at specific active site arginine residues occur in most low-grade gliomas, secondary glioblastomas, and in some acute myeloid leukemias (AML)[1-3]. These mutations alter IDH enzymatic function, resulting in the conversion of 2-oxoglutarate to the rare metabolite D-2-hydroxyglutarate (D-2-HG), which accumulates to high levels in cells and tissues[4,5]. D-2-HG may act as an oncometabolite, driving tumor progression by interfering with 2-oxoglutarate-dependent enzymes that affect hypoxia signalling (prolyl hydroxylases), histone methylation, and DNA methylation (TET2) [6,7]. Despite extensive genotyping, IDH1 and IDH2 mutations have not been identified in significant proportions of other neoplasms[3,8,9].

Peripheral T-cell lymphomas (PTCL) are non-Hodgkin lymphomas with a diverse presentation, histology, therapy response, and outcome[10]. Since this group of diseases has not been comprehensively assessed for the presence of IDH mutations, patient samples from three independent groups were genotyped to determine whether these mutations are present.

Methods

Patients and clinical data

Lymphoma and leukemia DNA samples from frozen tissue were provided by a multicentric T-cell lymphoma consortium (Tenomic) and the University of Hong Kong (UHK). Diagnosis was confirmed by a panel of pathologists to ensure consistent classification of PTCL according to the WHO classification.
A complimentary set of DNA from 22 angioimmunoblastic T-cell lymphomas (AITL) was provided by the University of Nebraska Medical Center (UNMC) Lymphoma Tumor Bank[11]. These AITL patients were identified by histopathologic assessment and confirmed by gene expression profiling[11].

As there is no standard therapy for AITL, patients received heterogeneous treatment. AITL samples with greater than 50% estimated tumor cell content were prioritized (**Table S1**). All patients provided informed consent in accordance with the Declaration of Helsinki.

IDH1 and IDH2 Genotyping

For Tenomic and UHK patients, IDH1 R132 and IDH2 R172 and R140 genotypes were determined at the Analytical Genetics Technology Centre at the University Health Network (Toronto, Canada) using a Sequenom MassARRAY™ platform (Sequenom, San Diego, CA) as previously described[5]. Positive results were confirmed by Sanger sequencing of the mutated region. In the UNMC patients, IDH1 and IDH2 genotype was determined by Sanger sequencing of all exons and subsequently by Sequenom (Genomic Core facility, UNMC, Omaha, NE). Sequenom genotyping is more sensitive and specific than Sanger sequencing, with the ability to detect a mutation in 10% of the input DNA, which is an advantage for samples with stromal contamination[12].

Statistical Analysis

Fisher's exact text and the Wilcoxon rank sum test were used to test for differences between IDH2wt and IDH2 mutant patients. Estimates of overall and progression-free survival were calculated using the Kaplan-Meier method, and compared using the log-rank test.

Results and Discussion

Lymphoma samples from the Tenomic consortium and HKU were genotyped to determine whether mutations were present in IDH1 at R132 and in IDH2 at R172 and R140 (**Table 1**). This set of samples included a large group of PTCL. Although other studies have suggested that IDH1/IDH2 mutations are not present in lymphomas and leukemias other than AML[3,9], PTCL has not been comprehensively studied.

No mutations were observed in lymphoma subtypes, including 46 B-cell lymphomas and 66 Hodgkin lymphomas, except for angioimmunoblastic T-cell lymphoma (AITL), where 16/79 (20%) samples from the Tenomic consortium carried an IDH2 mutation. This is the second common mutation to be identified in AITL after TET2[13], and makes AITL the third disease where IDH1/IDH2 mutations have been identified in a significant proportion of patients. As has been observed in glioma and AML, all mutations were heterozygous. However, the spectrum of mutations observed in AITL was different. Unlike in glioma and AML, no IDH1 mutations were identified, and the IDH2 mutations were largely confined to alterations resulting in an R172 substitution (12 R172K, 2 R172G, 1 R172T, and 1 R140G).

To further validate these results, 22 AITL patients from UNMC were genotyped (**Table 1**). None of the patients carried IDH1 mutations, and in 10/22 cases (45%) IDH2 mutations were identified, confirming the results of the Tenomic data. Although this was an independent set of patients, and mutation detection was performed using Sanger sequencing of all exons, the mutation spectrum was consistent with that of the Tenomic patients, with the IDH2 mutations detected at R172 (4 R172K, 4 R172S, 1 R172T and 1 R172G). There were no other mutations found in IDH1 or IDH2. The higher rate of mutation in this smaller set of patients may reflect differences in patient selection defined by a gene expression signature[11] which may identify a more homogeneous group of patients that share the IDH2 mutation at higher frequency.

AITL is one of the three most common PTCL subtypes, along with anaplastic large cell lymphoma and PTCL not otherwise specified[14]. It normally presents as a systemic disease, with polyadenopathy and a variety of immunologic abnormalities, and carries a poor prognosis[15]. Based on molecular marker expression (CD4, CD10, BCL6, PD1, CXCL13) and microarray profiling, AITL is thought to arise from follicular T-helper cells normally present in germinal centres[11,16,17]. The molecular pathogenesis and underlying genetic events driving AITL are largely unknown.

The clinical features of IDH2 wildtype and mutant AITL patients were assessed. Although all clinical parameters were not available for each patient, there were no significant differences between the two groups in the Tenomic patients, except that the Direct Coombs test was less frequently positive in IDH2 mutant patients (**Table S1**). These results were consistent with the smaller UNMC patient group (data not shown). Upon review, there were no pathological differences between the groups. Furthermore, IDH2 status had no effect on progression-free or overall survival (**Figure 1**). This is at odds with the findings in glioma, where IDH1/IDH2 mutations predict for improved survival, but more consistent with AML, where there is no overall independent impact on outcome, although some studies show prognostic value when specific IDH mutations are combined with other prognostic markers[18]. Prognostic impact may be difficult to detect in AITL, as patients are acquired from multiple centers and receive heterogeneous treatment.

Although the current results suggest that IDH2 may not provide prognostic information in AITL, a better understanding of the mechanisms underlying IDH1/IDH2 driven tumor progression may lead to new opportunities for AITL treatment. Future measurement of D-2-HG, the metabolite produced by these mutant enzymes, may provide a useful biomarker of disease progression and response to therapy. In addition, small molecule inhibitors specific for the mutant IDH2 enzymes could represent important tools in the future management of AITL.

Authorship

R.A.C., J.I., L.X., L.C.C., W.C., P.B., P.G. and T.W.M. designed the research. R.A.C., J.I., C.K., L.D.L., M.P., F.L., L.X. and A.M. performed research and collected and analyzed the data. F.L., J.P.J., and J.I. performed statistical analysis. R.A.C. wrote the manuscript.

The authors declare they have no competing conflicts of interest.

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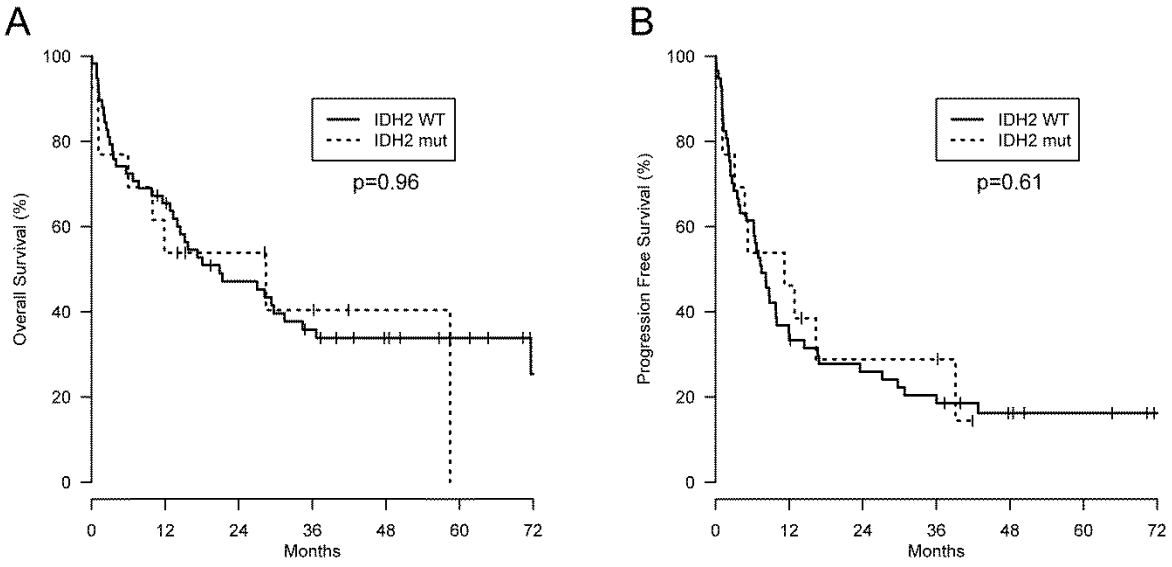
Table 1: IDH1 and IDH2 mutation status of lymphoma samples

Disease	IDH1R132	IDH2R172	IDH2R140
Tenomic consortium and UHK patients			
Hodgkin lymphoma	0/66	0/66	0/66
Non-hodgkin B-cell lymphoma	0/14	0/14	0/14
B-cell Acute lymphoblastic lymphoma (ALL B)	0/32	0/32	0/32
T-cell Acute lymphoblastic lymphoma (ALL T)	0/8	0/8	0/8
Acute myeloid leukemia (AML)	2/8	0/8	0/8
Peripheral T-cell Lymphomas (PTCL)			
PTCL not otherwise specified (PTCLnos)	0/43	0/43	0/43
Anaplastic large cell lymphoma (ALCL)	0/50	0/50	0/50
Enteropathy type T-cell lymphoma (ETL)	0/8	0/8	0/8
Cutaneous T-cell lymphoma (CTCL)	0/17	0/17	0/17
Hepatosplenic T-cell lymphoma (HSTCL)	0/10	0/10	0/10
Extranodal NK / T-cell lymphoma (NK/TCL)	0/10	0/10	0/10
Angioimmunoblastic T-cell lymphoma (AITL)	0/79	15/79	1/79
UNMC patients			
Angioimmunoblastic T-cell lymphoma (AITL)	0/22	10/22	0/22

Figure legends

Figure 1: Overall survival (A), and progression free survival (B) of AITL patients with wildtype (n=61) or mutant IDH2 (n=16) from the Tenomic consortium data set. Wildtype IDH2 patients were not significantly different from IDH2 mutant patients for either parameter.

Figure 1



Supplementary Materials and Methods

IDH1 and IDH2 Genotyping

DNA from fresh frozen and cryopreserved biopsies was extracted using QIAamp DNA mini kit or Quiagen Allprep kit (QIAGEN) according to the manufacturer's instructions. For AITL patients, samples were selected with > 50% tumor content as estimated by morphology, immunohistochemistry, and/or T-cell receptor clonality analysis (ie. single or biallelic peak is at least 5 times greater than polyclonal background)[1]. DNA was PCR amplified prior to Sequenom genotyping and Sanger sequencing using standard protocols. Amplification for Sequenom genotyping consisted of 10 ng DNA starting material and 45 cycles of (20s at 95C; 30s at 56 C; 60s at 72C). Amplification for Sanger sequencing consisted of 200 ng DNA starting material and 30 cycles of (20s at 95C; 20s at 64C; 45s at 72C). Sequences for PCR and Sequenom extension primers are defined below.

Primer sequences:

PCR Primers for Sequenom genotyping of IDH1 R132
ACGTTGGATGACATGACTTACTTGATCCCC
ACGTTGGATGAATATCCCCCGGCTTGTGAG
Sequenom Extension Primers for IDH1 R132
GATCCCCATAAGCATGA
ATCCCCATAAGCATGAC
PCR Primers for Sequenom genotyping of IDH2 R140
ACGTTGGATGTTTTTGCAGATGATGGGCTC
ACGTTGGATGGATGTGGAAAAGTCCCAATG
Sequenom Extension Primers for IDH2 R140
GATCCCCATAAGCATGA
ATCCCCATAAGCATGAC
PCR Primers for Sequenom genotyping of IDH2 R172
ACGTTGGATGTGGCCTACCTGGTCGCCAT
ACGTTGGATGAAAACATCCCACGCCTAGTC
Sequenom Extension Primers for IDH2 R172
CCCATCACCATTGGC
TCGCCATGGGCGTGC
PCR Primers for Sanger sequencing of IDH2 R172
GCCGCCTGCGGGGAAGTTGTACAC
CGTCTGGCTGTGTTGTTGCTTGGGG

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Table S1: Clinical data for IDH1/2 mutant and wild-type AITL patients from the Tenomic consortium

	IDH2 mutant (N=16)	IDH2 wildtype (N=63)	
Sex			
Male	8 (50%)	43 (68%)	p=0.24
Female	8 (50%)	20 (32%)	
Age (median)	72	69	p=0.52
Stage			
I-II	0 (0%)	3 (5%)	p=1
III-IV	12 (100%)	53 (95%)	
Percent tumor content			
>70%	2 (12%)	9 (15%)	p=1
50-70%	11 (69%)	34 (56%)	
30-50%	3 (19%)	16 (26%)	
0-30%	0 (0%)	2 (3%)	
Lactate dehydrogenase			
Elevated	11 (85%)	41 (77%)	p=0.72
Normal	2 (15%)	12 (23%)	
Hemoglobin			
>10g/dL	9 (69%)	36 (68%)	p=1
<10g/dL	4 (31%)	17 (32%)	
Platelet count			
>150000/mm3	11 (85%)	40 (75%)	p=0.71
<150000/mm3	2 (15%)	13 (25%)	
Direct Coombs test			
Positive	8 (100%)	19 (58%)	p=0.03
Negative	0 (0%)	14 (42%)	
Hypergammaglobulinemia			
Yes	4 (40%)	21 (47%)	p=0.74
No	6 (60%)	24 (53%)	
B symptoms			
Yes	8 (73%)	34 (69%)	p=1
No	3 (27%)	15 (31%)	
Performance status			
0-1	6 (55%)	22 (42%)	p=0.5
2-4	5 (45%)	31 (58%)	
International Prognostic Index			
0-1	1 (8%)	1 (2%)	p=0.67
2	2 (15%)	6 (12%)	
3	3 (23%)	17 (34%)	
4-5	7 (54%)	26 (52%)	
Prognostic Model for PTCLnos			
0-1	2 (15%)	5 (11%)	p=0.83
2	3 (23%)	12 (27%)	
3	6 (23%)	16 (36%)	
4	2 (15%)	11 (25%)	

Supplementary Appendix 1: TENOMIC consortium members

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